

Query= SEQ ID NO:3
 (1047 letters)

Sequences producing significant alignments: Score E
 (bits) Value

AC008121.33.67777.200926 546 e-153

>AC008121.33.67777.200926
 Length = 133150

Score = 546 bits (275), Expect = e-153
 Identities = 275/275 (100%)
 Strand = Plus / Plus

Query: 382 agcgatcctttaatgtggacagctgtgattggaactaataatatacatggacgctatcct 441
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 51038 agcgatcctttaatgtggacagctgtgattggaactaataatatacatggacgctatcct 51097

Query: 442 cataccaagaagataaaaaattaaagcaatcattattcatccaaacttcattttggaatct 501
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 Sbjct: 51098 cataccaagaagataaaaaattaaagcaatcattattcatccaaacttcattttggaatct 51157

Query: 502 tatgtaaatagatattgcactttttcacttaaaaaaagcagtgaggtataatgactatatt 561
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 51158 tatgtaaatagatattgcactttttcacttaaaaaaagcagtgaggtataatgactatatt 51217

Query: 562 cagcctatttgcctaccttttgatgttttcctgacggaacacaaagtgtttt 621
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Query: 622 ataagtggctggggaagaacaaaagaagaaggtaa 656
 ||||||||||||||||||||||||||||||||
 Sbjct: 51278 ataagtggctggggaagaacaaaagaagaaggtaa 51312

Score = 502 bits (253), Expect = e-139
 Identities = 253/253 (100%)
 Strand = Plus / Plus

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.....
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|||||
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Query: 975 acttactataaatattttacgtggccagatcctcatagctttatgttttgtcatcttact 1034
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Query: 1035 agcaacaacataa 1047
|||||
Sbjct: 79828 agcaacaacataa 79840

Score = 387 bits (195), Expect = e-105
Identities = 196/197 (99%)
Strand = Plus / Plus

Query: 187 gattgtggaacagcaccgcttaaggatgtgttgcaagggtctcggattatagggggcacc 246
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Query: 247 gaagcacaagctggcgcatggccgtgggtggtgagcctgcagattaaatatggccgtgtt 306
|||||
Sbjct: 36151 gaagcacaagctggcgcatggccgtgggtggtgagcctgcagattaaatatggccgtgtt 36210

Query: 307 cttgttcatgtatgtgggggaaccctagtgtgagagagaggtgggtcctcacagctgccac 366
|||||
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Query: 367 tgcactaaagacrctag 383
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Score = 363 bits (183), Expect = 9e-98
Identities = 185/187 (98%)
Strand = Plus / Plus

Query: 1 atgcggctggggctcctgagcgtggcgytggttgtttgtggggagctctcacttayactca 60
|||||

Sbjct: 35275 gaccaactactcgccctctggaaggcacaggtcggccctcgccggaaccggcggtagt 35334

Query: 121 tcccagcaggctgaggccgtccgcaagaggctccggcggcggagggagggaggggcgcat 180
|||||
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Query: 181 gcaaagg 187
|||||
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Score = 290 bits (146), Expect = 1e-75
Identities = 146/146 (100%)
Strand = Plus / Plus

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Query: 711 taattctgagaggagttatgggggaataattcctaacacttcattttgtgcaggtgatga 770
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Query: 771 agatggagcttttgatacttgcaggg 796
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Sbjct: 77691 agatggagcttttgatacttgcaggg 77716



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1: AC008121. Homo sapiens 12 B...[gi:28626577]

Links

LOCUS AC008121 105989 bp DNA linear PRI 01-MAR-2003

DEFINITION Homo sapiens 12 BAC RP11-407N8 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

ACCESSION AC008121

VERSION AC008121.43 GI:28626577

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 105989)

AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S.,
Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P.,
Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N.,
Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P.,
Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M.,
Holloway,C., Hollins,B., Homsy,F., Howard,S., Huber,J., Hulyk,S.,
Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y.,
Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U.,
King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N.,
Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O.,
Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X.,
Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P.,
Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E.,
Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S.,

Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,C., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Sharma,S., Smith,E., Smith,H., Smith,J., Smith,K., Smith,L.,
Smith,M., Smith,N., Smith,O., Smith,P., Smith,Q., Smith,R.,
Smith,S., Smith,T., Smith,U., Smith,V., Smith,W., Smith,X.,
Smith,Y., Smith,Z., Smith,AA, Smith,AB, Smith,AC, Smith,AD, Smith,AE,

>XM_171629 ACCESSION:XM_171629 NID: gi 22062231 ref XM_171629.1 Homo
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 precursor (LOC257238), mRNA
 Length = 1295

Identities = 141/153 (92%), Positives = 141/153 (92%)
 Frame = +3

Query: 62 CGTAPLKDVLQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRERWVLTAAHC 121
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 Sbjct: 3 CGTAPLKDVLQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRE----- 155

Query: 122 TKDSDPLMWTAVIGTNNIHGRYPHTKKIKIKAIHHPNFILESVNDIALFHLKKAVRYN 181
 SDPLMWTAVIGTNNIHGRYPHTKKIKIKAIHHPNFILESVNDIALFHLKKAVRYN
 Sbjct: 156 ---SDPLMWTAVIGTNNIHGRYPHTKKIKIKAIHHPNFILESVNDIALFHLKKAVRYN 326

Query: 182 DYIQPICLPFDVQILDGNTKCFISGWGRTKEE 214
 DYIQPICLPFDVQILDGNTKCFISGWGRTKEE
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Identities = 131/131 (100%), Positives = 131/131 (100%)
 Frame = +3

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 Sbjct: 900 GNATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP 1079

Query: 275 EYKRFFVMGITSYGHGCGRRGFPVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 334
 EYKRFFVMGITSYGHGCGRRGFPVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI
 Sbjct: 1080 EYKRFFVMGITSYGHGCGRRGFPVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 1259

Query: 335 ALCFVILLATT 345
 ALCFVILLATT
 Sbjct: 1260 ALCFVILLATT 1292



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1: XM_171629. Homo sapiens simi...[gi:22062231]

Links

LOCUS LOC257238 1295 bp mRNA linear PRI 01-AUG-2002

DEFINITION Homo sapiens similar to cortical granule serine protease 1 precursor (LOC257238), mRNA.

ACCESSION XM_171629

VERSION XM_171629.1 GI:22062231

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1295)

AUTHORS NCBI Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-2002) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was predicted from NCBI contig NT_009782 by automated computational analysis using gene prediction method: GenomeScan, supported by EST evidence.

Also see:

[Documentation](#) of NCBI's Annotation Process

FEATURES

source Location/Qualifiers

1..1295

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/chromosome="12"

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/protein_id="XP_171629.1"

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1144

gene="LOC257238"

/note="Region: smart00020, Tryp_SPC, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

misc_feature 171..434

/gene="LOC257238"

/note="Region: pfam00089, trypsin, Trypsin"

misc_feature 819..1199

/gene="LOC257238"

/note="Region: pfam02395, IGA1, Immunoglobulin A1 protease. This family consists of immunoglobulin A1 protease proteins. The immunoglobulin A1 protease cleaves immunoglobulin IgA and is found in pathogenic bacteria such as Neisseria gonorrhoeae. Not all of the members of this family are IgA proteases (one member from E. coli cleaves human coagulation factor V, another one is a hemoglobin protease)"

misc_feature 900..1187

/gene="LOC257238"

/note="Region: smart00020, Tryp_SPC, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

misc_feature 903..1187

/gene="LOC257238"

/note="Region: pfam00089, trypsin, Trypsin"

variation

681

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/allele="C"

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BASE COUNT 352 a 265 c 314 g 364 t

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121 ttgttcatgt atgtggggga accctagtga gagagagcga tcctttaatg tggacagctg
181 tgattggaac taataatata catggacgct atcctcatac caagaagata aaaattaaag
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301 acttaaaaaa agcagtgagg tataatgact atattcagcc tatttgecta cttttgatg
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421 aagaaggtat agcaggcttt gtgactgtgg tgtcctgtgg tctttacaag ctaaagtaca
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1021 atggagcttt tgataacttg aggggtgaca gtgggggacc attaattgtc tacttaccag
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1201 tttttttt gttttttt gttttttt gttttttt gttttttt gttttttt
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1261 ctttatgttt tgtcatttta ctagcaacaa cataa
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Revised: July 5, 2002.

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Dec 2 2002 13:45:47

>XM_208689 ACCESSION:XM_208689 NID: gi 30157117 ref XM_208689.3
Homo sapiens similar to adrenal secretory serine
protease precursor (LOC283471), mRNA
Length = 1457

Score = 712 bits (1819), Expect = 0.0
Identities = 344/348 (98%), Positives = 345/348 (98%), Gaps = 3/348 (0%)
Frame = +1

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Sbjct: 40 MRLGLLSVALLFVGSSHLSDHYSPSGRHRRLGPSPEPAASSQAEAVRKRLRRRREGGAH 219

Query: 59 AKDCGTAPLKDV LQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRERWVLTA 118
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Query: 119 AHCTKD-SDPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKA 177
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Sbjct: 400 AHCTKDASDPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKA 579

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Query: 238 RSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLPEYKRFFVMGITSYGHGCGRRGFP 297
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Query: 298 GVIYIGPSFYQKWLTEHFFHASTQGILTINILRGQILIALCFVILLATT 345
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Boo

Clear

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Links

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[illegible]

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turnover, chaperones]"
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May 2 2003 16:47:12